

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 09/709,585

Source: _____

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IFW16

RAW SEQUENCE LISTING

DATE: 05/16/2005

PATENT APPLICATION: US/09/709,585

TIME: 11:32:15

Input Set : N:\Crf3\RULE60\09709585.raw.txt

Output Set: N:\CRF4\05162005\I709585.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Vinik, Aaron I.

6 Pittenger, Gary L.

7 Rafaeloff, Ronit

8 Rosenberg, Lawrence

9 Duguid, William P.

11 (ii) TITLE OF INVENTION: INGAP PROTEIN INVOLVED IN PANCREATIC
12 ISLET NEOGENESIS

14 (iii) NUMBER OF SEQUENCES: 7

16 (iv) CORRESPONDENCE ADDRESS:

17 (A) ADDRESSEE: Banner & Allegretti

18 (B) STREET: 1001 G Street, N.W.

19 (C) CITY: Washington

20 (D) STATE: D.C.

21 (E) COUNTRY: US

22 (F) ZIP: 20001-4597

24 (v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Floppy disk

26 (B) COMPUTER: IBM PC compatible

27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

30 (vi) CURRENT APPLICATION DATA:

C--> 31 (A) APPLICATION NUMBER: US/09/709,585

C--> 32 (B) FILING DATE: 13-Nov-2000

W--> 38 (C) CLASSIFICATION:

35 (vii) PRIOR APPLICATION DATA:

36 (A) APPLICATION NUMBER: US/08/401,530

37 (B) FILING DATE: 24-OCT-1996

40 (viii) ATTORNEY/AGENT INFORMATION:

41 (A) NAME: Kagan, Sarah A.

42 (B) REGISTRATION NUMBER: 32,141

43 (C) REFERENCE/DOCKET NUMBER: 00570.48743

45 (ix) TELECOMMUNICATION INFORMATION:

46 (A) TELEPHONE: 202-508-9100

47 (B) TELEFAX: 202-508-9299

50 (2) INFORMATION FOR SEQ ID NO: 1:

52 (i) SEQUENCE CHARACTERISTICS:

53 (A) LENGTH: 747 base pairs

54 (B) TYPE: nucleic acid

55 (C) STRANDEDNESS: single

56 (D) TOPOLOGY: linear

58 (ii) MOLECULE TYPE: cDNA

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60      (iii) HYPOTHETICAL: NO
62      (iv) ANTI-SENSE: NO
64      (vi) ORIGINAL SOURCE:
65          (A) ORGANISM: Cricetulus
67      (ix) FEATURE:
68          (A) NAME/KEY: CDS
69          (B) LOCATION: 20..541
72      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
74 CTGCAAGACA GGTACCATG ATG CTT CCC ATG ACC CTC TGT AGG ATG TCT TGG      52
75          Met Leu Pro Met Thr Leu Cys Arg Met Ser Trp
76          1          5          10
78 ATG CTG CTT TCC TGC CTG ATG TTC CTT TCT TGG GTG GAA GGT GAA GAA      100
79 Met Leu Leu Ser Cys Leu Met Phe Leu Ser Trp Val Glu Gly Glu Glu
80          15          20          25
82 TCT CAA AAG AAA CTG CCT TCT TCA CGT ATA ACC TGT CCT CAA GGC TCT      148
83 Ser Gln Lys Lys Leu Pro Ser Ser Arg Ile Thr Cys Pro Gln Gly Ser
84          30          35          40
86 GTA GCC TAT GGG TCC TAT TGC TAT TCA CTG ATT TTG ATA CCA CAG ACC      196
87 Val Ala Tyr Gly Ser Tyr Cys Tyr Ser Leu Ile Leu Ile Pro Gln Thr
88          45          50          55
90 TGG TCT AAT GCA GAA CTA TCC TGC CAG ATG CAT TTC TCA GGA CAC CTG      244
91 Trp Ser Asn Ala Glu Leu Ser Cys Gln Met His Phe Ser Gly His Leu
92 60          65          70          75
94 GCA TTT CTT CTC AGT ACT GGT GAA ATT ACC TTC GTG TCC TCC CTT GTG      292
95 Ala Phe Leu Leu Thr Gly Glu Ile Thr Phe Val Ser Ser Leu Val
96          80          85          90
98 AAG AAC AGT TTG ACG GCC TAC CAG TAC ATC TGG ATT GGA CTC CAT GAT      340
99 Lys Asn Ser Leu Thr Ala Tyr Gln Tyr Ile Trp Ile Gly Leu His Asp
100          95          100          105
102 CCC TCA CAT GGT ACA CTA CCC AAC GGA AGT GGA TGG AAG TGG AGC AGT      388
103 Pro Ser His Gly Thr Leu Pro Asn Gly Ser Gly Trp Lys Trp Ser Ser
104          110          115          120
106 TCC AAT GTG CTG ACC TTC TAT AAC TGG GAG AGG AAC CCC TCT ATT GCT      436
107 Ser Asn Val Leu Thr Phe Tyr Asn Trp Glu Arg Asn Pro Ser Ile Ala
108          125          130          135
110 GCT GAC CGT GGT TAT TGT GCA GTT TTG TCT CAG AAA TCA GGT TTT CAG      484
111 Ala Asp Arg Gly Tyr Cys Ala Val Leu Ser Gln Lys Ser Gly Phe Gln
112 140          145          150          155
114 AAG TGG AGA GAT TTT AAT TGT GAA AAT GAG CTT CCC TAT ATC TGC AAA      532
115 Lys Trp Arg Asp Phe Asn Cys Glu Asn Glu Leu Pro Tyr Ile Cys Lys
116          160          165          170
118 TTC AAG GTC TAGGGCAGTT CTAATTTCAA CAGAGAGCAA GCTCTGCCTA CACACCCACA      591
119 Phe Lys Val
122 CCAATTCCCT TATATCATCT CTGCTGTTTT TCCTTGAAAT TATTATGAAG CTCACATGGA      651
125 CAAGGAAGCA AGTATGAGGA TTCACTCAGG ATATCAGTAT ATTCTGTGGT GGCTGTAACC      711
128 TAAAGGCTCA GAGAACAAAA ATAAATGTC ATCAAC      747
131 (2) INFORMATION FOR SEQ ID NO: 2:
133      (i) SEQUENCE CHARACTERISTICS:
134          (A) LENGTH: 174 amino acids

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135          (B) TYPE: amino acid
136          (D) TOPOLOGY: linear
138          (ii) MOLECULE TYPE: protein
140          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
142 Met Leu Pro Met Thr Leu Cys Arg Met Ser Trp Met Leu Leu Ser Cys
143   1      5      10      15
145 Leu Met Phe Leu Ser Trp Val Glu Gly Glu Ser Gln Lys Lys Leu
146      20      25      30
148 Pro Ser Ser Arg Ile Thr Cys Pro Gln Gly Ser Val Ala Tyr Gly Ser
149      35      40      45
151 Tyr Cys Tyr Ser Leu Ile Leu Ile Pro Gln Thr Trp Ser Asn Ala Glu
152   50      55      60
154 Leu Ser Cys Gln Met His Phe Ser Gly His Leu Ala Phe Leu Leu Ser
155  65      70      75      80
157 Thr Gly Glu Ile Thr Phe Val Ser Ser Leu Val Lys Asn Ser Leu Thr
158      85      90      95
160 Ala Tyr Gln Tyr Ile Trp Ile Gly Leu His Asp Pro Ser His Gly Thr
161      100     105     110
163 Leu Pro Asn Gly Ser Gly Trp Lys Trp Ser Ser Ser Asn Val Leu Thr
164      115     120     125
166 Phe Tyr Asn Trp Glu Arg Asn Pro Ser Ile Ala Ala Asp Arg Gly Tyr
167      130     135     140
169 Cys Ala Val Leu Ser Gln Lys Ser Gly Phe Gln Lys Trp Arg Asp Phe
170 145     150     155     160
172 Asn Cys Glu Asn Glu Leu Pro Tyr Ile Cys Lys Phe Lys Val
173      165     170
175 (2) INFORMATION FOR SEQ ID NO: 3:
177   (i) SEQUENCE CHARACTERISTICS:
178       (A) LENGTH: 175 amino acids
179       (B) TYPE: amino acid
180       (D) TOPOLOGY: linear
182   (ii) MOLECULE TYPE: protein
184   (iv) ANTI-SENSE: NO
186   (vi) ORIGINAL SOURCE:
187       (A) ORGANISM: Rattus rattus
190   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
192 Met Leu His Arg Leu Ala Phe Pro Val Met Ser Trp Met Leu Leu Ser
193   1      5      10      15
195 Cys Leu Met Leu Leu Ser Gln Val Gln Gly Glu Asp Ser Pro Lys Lys
196      20      25      30
198 Ile Pro Ser Ala Arg Ile Ser Cys Pro Lys Gly Ser Gln Ala Tyr Gly
199      35      40      45
201 Ser Tyr Cys Tyr Ala Leu Phe Gln Ile Pro Gln Thr Trp Phe Asp Ala
202   50      55      60
204 Glu Leu Ala Cys Gln Lys Arg Pro Glu Gly His Leu Val Ser Val Leu
205  65      70      75      80
207 Asn Val Ala Glu Ala Ser Phe Leu Ala Ser Met Val Lys Asn Thr Gly
208      85      90      95
210 Asn Ser Tyr Gln Tyr Ile Trp Ile Gly Leu His Asp Pro Thr Leu Gly

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211		100		105		110
213	Gly	Glu	Pro	Asn	Gly	Gly
214		115		120		125
216	Asn	Tyr	Val	Asn	Trp	Glu
217		130		135		140
219	Phe	Cys	Gly	Ser	Leu	Ser
220		145		150		155
222	Thr	Thr	Cys	Glu	Val	Lys
223		165		170		175

225 (2) INFORMATION FOR SEQ ID NO: 4:

227 (i) SEQUENCE CHARACTERISTICS:

228 (A) LENGTH: 175 amino acids

229 (B) TYPE: amino acid

230 (D) TOPOLOGY: linear

232 (ii) MOLECULE TYPE: protein

234 (vi) ORIGINAL SOURCE:

235 (A) ORGANISM: Homo sapiens

238 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

240	Met	Leu	Pro	Pro	Met	Ala	Leu	Pro	Ser	Val	Ser	Trp	Met	Leu	Leu	Ser
241	1				5				10					15		
243	Cys	Leu	Met	Leu	Leu	Ser	Gln	Val	Gln	Gly	Glu	Glu	Pro	Gln	Arg	Glu
244				20				25					30			
246	Leu	Pro	Ser	Ala	Arg	Ile	Arg	Cys	Pro	Lys	Gly	Ser	Lys	Ala	Tyr	Gly
247			35				40					45				
249	Ser	His	Cys	Tyr	Ala	Leu	Phe	Leu	Ser	Pro	Lys	Ser	Trp	Thr	Asp	Ala
250		50				55				60						
252	Asp	Leu	Ala	Cys	Gln	Lys	Arg	Pro	Ser	Gly	Asn	Leu	Val	Ser	Val	Leu
253	65				70				75					80		
255	Ser	Gly	Ala	Glu	Gly	Ser	Phe	Val	Ser	Ser	Leu	Val	Lys	Ser	Ile	Gly
256				85				90					95			
258	Asn	Ser	Tyr	Ser	Tyr	Val	Trp	Ile	Gly	Leu	His	Asp	Pro	Thr	Gln	Gly
259			100					105					110			
261	Thr	Glu	Pro	Asn	Gly	Glu	Gly	Trp	Glu	Trp	Ser	Ser	Ser	Asp	Val	Met
262			115				120					125				
264	Asn	Tyr	Phe	Ala	Trp	Glu	Arg	Asn	Pro	Ser	Thr	Ile	Ser	Ser	Pro	Gly
265		130				135					140					
267	His	Cys	Ala	Ser	Leu	Ser	Arg	Ser	Thr	Ala	Phe	Leu	Arg	Trp	Lys	Asp
268		145			150					155				160		
270	Tyr	Asn	Cys	Asn	Val	Arg	Leu	Pro	Tyr	Val	Cys	Lys	Phe	Thr	Asp	
271			165				170						175			

273 (2) INFORMATION FOR SEQ ID NO: 5:

275 (i) SEQUENCE CHARACTERISTICS:

276 (A) LENGTH: 174 amino acids

277 (B) TYPE: amino acid

278 (D) TOPOLOGY: linear

280 (ii) MOLECULE TYPE: protein

282 (vi) ORIGINAL SOURCE:

283 (A) ORGANISM: Rattus rattus

286 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

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288 Met Leu Pro Arg Val Ala Leu Thr Thr Met Ser Trp Met Leu Leu Ser
289 1 5 10 15
291 Ser Leu Met Leu Leu Ser Gln Val Gln Gly Glu Asp Ala Lys Glu Asp
292 20 25 30
294 Val Pro Thr Ser Arg Ile Ser Cys Pro Lys Gly Ser Arg Ala Tyr Gly
295 35 40 45
297 Ser Tyr Cys Tyr Ala Leu Phe Ser Val Ser Lys Ser Trp Phe Asp Ala
298 50 55 60
300 Asp Leu Ala Cys Gln Lys Arg Pro Ser Gly His Leu Val Ser Val Leu
301 65 70 75 80
303 Ser Gly Ser Glu Ala Ser Phe Val Ser Ser Leu Ile Lys Ser Ser Gly
304 85 90 95
306 Asn Ser Gly Gln Asn Val Trp Ile Gly Leu His Asp Pro Thr Leu Gly
307 100 105 110
309 Gln Glu Pro Asn Arg Gly Gly Trp Glu Trp Ser Asn Ala Asp Val Met
310 115 120 125
312 Asn Tyr Phe Asn Trp Glu Thr Asn Pro Ser Ser Val Ser Gly Ser His
313 130 135 140
315 Cys Gly Thr Leu Thr Arg Ala Ser Gly Phe Leu Arg Trp Arg Glu Asn
316 145 150 155 160
318 Asn Cys Ile Ser Glu Leu Pro Tyr Val Cys Lys Phe Lys Ala
319 165 170

```

321 (2) INFORMATION FOR SEQ ID NO: 6:

323 (i) SEQUENCE CHARACTERISTICS:

324 (A) LENGTH: 174 amino acids

325 (B) TYPE: amino acid

326 (D) TOPOLOGY: linear

328 (ii) MOLECULE TYPE: protein

330 (vi) ORIGINAL SOURCE:

331 (A) ORGANISM: Rattus rattus

334 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```

336 Met Leu Pro Arg Leu Ser Phe Asn Asn Val Ser Trp Thr Leu Leu Tyr
337 1 5 10 15
339 Tyr Leu Phe Ile Phe Gln Val Arg Gly Glu Asp Ser Gln Lys Ala Val
340 20 25 30
342 Pro Ser Thr Arg Thr Ser Cys Pro Met Gly Ser Lys Ala Tyr Arg Ser
343 35 40 45
345 Tyr Cys Tyr Thr Leu Val Thr Thr Leu Lys Ser Trp Phe Gln Ala Asp
346 50 55 60
348 Leu Ala Cys Gln Lys Arg Pro Ser Gly His Leu Val Ser Ile Leu Ser
349 65 70 75 80
351 Gly Gly Glu Ala Ser Phe Val Ser Ser Leu Val Thr Gly Arg Val Asn
352 85 90 95
354 Asn Asn Gln Asp Ile Trp Ile Trp Leu His Asp Pro Thr Met Gly Gln
355 100 105 110
357 Gln Pro Asn Gly Gly Gly Trp Glu Trp Ser Asn Ser Asp Val Leu Asn
358 115 120 125
360 Tyr Leu Asn Trp Asp Gly Asp Pro Ser Ser Thr Val Asn Arg Gly Asn
361 130 135 140

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/709,585

DATE: 05/16/2005

TIME: 11:32:16

Input Set : N:\Crf3\RULE60\09709585.raw.txt

Output Set: N:\CRF4\05162005\I709585.raw

L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:38 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)